



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 152115

TO: Nita M Minnifield
Location: REM-3C01&3C18

Art Unit: 1645

May 3, 2005

Case Serial Number: 09/642744

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

*Reviewed
6-5-05*

152115

From: Chan, Christina
Sent: Friday, April 29, 2005 3:42 PM
To: Pak, Michael; STIC-Biotech/ChemLib
Cc: Minnifield, Nita
Subject: RE: approval for additional sequences to be searched

Importance: High

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFE

-----Original Message-----

From: Pak, Michael
Sent: Friday, April 29, 2005 1:37 PM
To: Chan, Christina
Cc: Minnifield, Nita
Subject: RE: approval for additional sequences to be searched

Dear STIC,

Please search the multiple sequence search request set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Minnifield, Nita
Sent: Thursday, April 28, 2005 10:09 PM
To: Pak, Michael
Subject: approval for additional sequences to be searched

Michael,
09/642744

I have been asked to work on this application (originally not my case) since it is an AF that is overdue and Atty. is calling regarding response to the AF and his time is running out. All of the sequences were searched previously, but they need to be searched again because Applicant corrected some error that was in the RSL.

SEQ ID NO: 1, 6-17, 19-26 and 28. They are all peptides. I need a commercial and interference search done.

Your approval is greatly appreciated.

Please forward to Christina for RUSH approval.

STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

09/642744

Please do a commercial and interference search on SEQ ID NO: 1, 6-17, 19-26 and 28. They are all peptides.

Please provide a paper copy of results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51 ; Search time 93.3333 Seconds
(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744d-7
Perfect score: 90
Sequence: 1 KNIRRIKRIHIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	61.1	160	1	SCS1_SHEEP
2	55	61.1	160	1	SCS2_SHEEP
3	52	57.8	146	2	09A1H3
4	49	54.4	2017	2	0675T1
5	48.5	53.9	314	2	065L76
6	48.5	53.9	324	2	062X75
7	48	53.3	255	2	09LJW2
8	48	53.3	500	1	TF3B_SCHPO
9	47	52.2	232	2	07MTQ1
10	47	52.2	581	2	06EBB6
11	47	52.2	3267	2	081B20
12	46	51.1	93	2	064D16
13	46	51.1	113	2	0703Z0
14	46	51.1	250	2	06L7F9
15	46	51.1	282	2	08DVR3
16	46	51.1	282	2	08B4C0
17	46	51.1	319	2	005804
18	46	51.1	343	2	076C22
19	46	51.1	807	1	HIS8_PHOLL
20	46	51.1	1774	2	0754J8
21	46	51.1	2084	2	081LJ6
22	45.5	50.6	208	1	TRP_NEMA
23	45.5	50.6	208	1	TRP_NEMA
24	45	50.0	182	2	0896E1
25	45	50.0	234	2	059264
26	45	50.0	308	2	08R2C7
27	45	50.0	420	1	PR11_HUMAN
28	45	50.0	609	2	072K21
29	45	50.0	609	2	08F9Q8
30	45	50.0	647	2	062647
31	45	50.0	834	2	07RR10

ALIGNMENTS

32	45	50.0	1160	2	08IM12	08im12 plasmodium
33	45	50.0	1634	1	DPOL_METUA	08a295 methanococc
34	44	48.9	78	2	08ZYK7	08zyk7 pyrobaculum
35	44	48.9	93	1	Y435_METUA	057877 methanococc
36	44	48.9	124	2	0649W3	0649w3 uncultured
37	44	48.9	125	2	064EA5	064ea5 uncultured
38	44	48.9	165	2	081B86	081b86 plasmodium
39	44	48.9	231	2	08RAG4	08rag4 thermoaer
40	44	48.9	233	2	09L7X2	09l7x2 clostridium
41	44	48.9	233	2	08XJ18	08xj18 clostridium
42	44	48.9	291	2	0738Z6	0738z6 bacillus ce
43	44	48.9	301	2	06H2B4	06h2b4 bacillus ce
44	44	48.9	301	2	063BX5	063bx5 bacillus an
45	44	48.9	301	2	081E24	081e24 bacillus ce

RESULT 1
SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SNAP-29) (Weiloid antibacterial peptide SNAP-29).
OS Ovis aries (sheep).
OC Buxarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RA Mahoney M.M., Lee A.Y., Brezinski-Caliquiri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel antimicrobial peptide."
RL FEBS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Huttner K.M., Mahoney M.M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Thermolabile, broad spectrum, bactericidal agent.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X92757; CAAG3412.1; -
DR EMBL: U60600; AAB89715.1; -
DR PDB: 1FRY; NMR; A-132-160.
DR InterPro: IPR001894; Cathelicidin.
DR Pfam: PF00666; Cathelicidins; 1.
DR ProDom: PD001838; Cathelicidin; 1.
DR PROSITE: PS00946; CATHELICIDINS_1; 1.
DR PROSITE: PS00947; CATHELICIDINS_2; 1.
KM 3D-structure; Antibiotic; Pyroglutamate carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 131
FT PEPTIDE 132 160
FT MOD_RES 30 30
FT FT
FT DISULFID 86 97
FT By similarity.
FT By similarity.
FT By similarity.
FT By similarity.
FT By similarity.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 / Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744D-7
Perfect score: 90
Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	18	US-10-060-102-10	Sequence 10, Appl
2	90	100.0	18	US-10-060-102-11	Sequence 11, Appl
3	90	100.0	18	US-10-721-839-10	Sequence 10, Appl
4	90	100.0	18	US-10-721-839-11	Sequence 11, Appl
5	88	97.8	18	US-09-840-009-2	Sequence 2, Appl
6	88	97.8	18	US-09-840-009-9	Sequence 9, Appl
7	88	97.8	18	US-09-840-009-16	Sequence 16, Appl
8	88	97.8	18	US-09-840-009-23	Sequence 23, Appl
9	88	97.8	18	US-09-840-009-30	Sequence 30, Appl
10	88	97.8	18	US-10-060-102-9	Sequence 9, Appl
11	88	97.8	18	US-10-060-102-12	Sequence 12, Appl
12	88	97.8	18	US-10-721-839-9	Sequence 9, Appl
13	88	97.8	18	US-10-721-839-12	Sequence 12, Appl

14	88	97.8	29	14	US-10-060-102-8	Sequence 8, Appl
15	88	97.8	29	15	US-10-721-839-8	Sequence 8, Appl
16	83	92.2	18	9	US-09-840-009-4	Sequence 4, Appl
17	83	92.2	18	9	US-09-840-009-8	Sequence 8, Appl
18	83	92.2	18	9	US-09-840-009-11	Sequence 11, Appl
19	83	92.2	18	9	US-09-840-009-15	Sequence 15, Appl
20	83	92.2	18	9	US-09-840-009-18	Sequence 18, Appl
21	83	92.2	18	9	US-09-840-009-22	Sequence 22, Appl
22	83	92.2	18	9	US-09-840-009-25	Sequence 25, Appl
23	83	92.2	18	9	US-09-840-009-29	Sequence 29, Appl
24	83	92.2	18	14	US-10-060-102-25	Sequence 25, Appl
25	83	92.2	18	15	US-10-721-839-25	Sequence 25, Appl
26	82	91.1	18	9	US-09-840-009-5	Sequence 5, Appl
27	82	91.1	18	9	US-09-840-009-12	Sequence 12, Appl
28	82	91.1	18	9	US-09-840-009-19	Sequence 19, Appl
29	82	91.1	18	9	US-09-840-009-26	Sequence 26, Appl
30	81	90.0	18	9	US-09-840-009-6	Sequence 6, Appl
31	81	90.0	18	9	US-09-840-009-7	Sequence 7, Appl
32	81	90.0	18	9	US-09-840-009-13	Sequence 13, Appl
33	81	90.0	18	9	US-09-840-009-14	Sequence 14, Appl
34	81	90.0	18	9	US-09-840-009-20	Sequence 20, Appl
35	81	90.0	18	9	US-09-840-009-21	Sequence 21, Appl
36	81	90.0	18	9	US-09-840-009-27	Sequence 27, Appl
37	81	90.0	18	9	US-09-840-009-28	Sequence 28, Appl
38	80	88.9	18	9	US-09-840-009-3	Sequence 3, Appl
39	80	88.9	18	9	US-09-840-009-10	Sequence 10, Appl
40	80	88.9	18	9	US-09-840-009-17	Sequence 17, Appl
41	80	88.9	18	9	US-09-840-009-24	Sequence 24, Appl
42	80	88.9	18	9	US-09-840-009-31	Sequence 31, Appl
43	80	88.9	18	14	US-10-060-102-26	Sequence 26, Appl
44	80	88.9	18	14	US-10-077-624-17	Sequence 17, Appl
45	80	88.9	18	15	US-10-721-839-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-10
Sequence 10, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-10

Query Match 100.0%; Score 90; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNIRRIIRKIHIIKKYG 18

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32 ; Search time 25.6667 Seconds

(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-7

Sequence: 1 KNIRRIIRKIHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	97.8	18	US-09-840-009-2	Sequence 2, Appl
2	88	97.8	18	US-09-840-009-9	Sequence 9, Appl
3	88	97.8	18	US-09-840-009-16	Sequence 16, Appl
4	88	97.8	18	US-09-840-009-23	Sequence 23, Appl
5	88	97.8	18	US-09-840-009-30	Sequence 30, Appl
6	83	92.2	18	US-09-840-009-4	Sequence 4, Appl
7	83	92.2	18	US-09-840-009-8	Sequence 8, Appl
8	83	92.2	18	US-09-840-009-11	Sequence 11, Appl
9	83	92.2	18	US-09-840-009-15	Sequence 15, Appl
10	83	92.2	18	US-09-840-009-18	Sequence 18, Appl
11	83	92.2	18	US-09-840-009-22	Sequence 22, Appl
12	83	92.2	18	US-09-840-009-25	Sequence 25, Appl
13	83	92.2	18	US-09-840-009-29	Sequence 29, Appl
14	82	91.1	18	US-09-840-009-5	Sequence 5, Appl
15	82	91.1	18	US-09-840-009-12	Sequence 12, Appl
16	82	91.1	18	US-09-840-009-19	Sequence 19, Appl
17	82	91.1	18	US-09-840-009-26	Sequence 26, Appl
18	81	90.0	18	US-09-840-009-6	Sequence 6, Appl
19	81	90.0	18	US-09-840-009-13	Sequence 13, Appl
20	81	90.0	18	US-09-840-009-20	Sequence 20, Appl
21	81	90.0	18	US-09-840-009-14	Sequence 14, Appl
22	81	90.0	18	US-09-840-009-21	Sequence 21, Appl
23	81	90.0	18	US-09-840-009-27	Sequence 27, Appl
24	81	90.0	18	US-09-840-009-28	Sequence 28, Appl
25	81	90.0	18	US-09-840-009-3	Sequence 3, Appl
26	80	88.9	18	US-09-840-009-3	Sequence 10, Appl
27	80	88.9	18	US-09-840-009-3	Sequence 10, Appl

28	80	88.9	18	US-09-840-009-17	Sequence 17, Appl
29	80	88.9	18	US-09-840-009-24	Sequence 24, Appl
30	80	88.9	18	US-09-840-009-31	Sequence 31, Appl
31	74	82.2	18	US-09-840-009-34	Sequence 34, Appl
32	74	82.2	18	US-09-840-009-35	Sequence 35, Appl
33	72	80.0	18	US-09-840-009-32	Sequence 32, Appl
34	72	80.0	18	US-09-840-009-33	Sequence 33, Appl
35	68	75.6	18	US-09-840-009-1	Sequence 1, Appl
36	63	70.0	18	US-09-840-009-36	Sequence 36, Appl
37	63	70.0	18	US-09-840-009-37	Sequence 37, Appl
38	55	61.1	160	US-09-917-340-36	Sequence 36, Appl
39	52	57.8	169	US-09-270-767-35406	Sequence 37, Appl
40	52	57.8	169	US-09-270-767-35406	Sequence 36, Appl
41	48	53.3	205	US-09-134-001C-4766	Sequence 50623, A
42	44	48.9	24	US-09-785-059B-5	Sequence 4766, Ap
43	44	48.9	36	US-09-785-059B-6	Sequence 5, Appl
44	44	48.9	42	US-09-785-059B-7	Sequence 6, Appl
45	44	48.9	48	US-09-785-059B-8	Sequence 7, Appl
			4	US-09-785-059B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2

Sequence 2, Application US/09840009
Patent No. 6492328

GENERAL INFORMATION:

APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.

APPLICANT: Tack, Brian F.

TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES

FILE REFERENCE: 06510-195WO

CURRENT APPLICATION NUMBER: US/09/840,009

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic antimicrobial peptide

US-09-840-009-2

Query Match

Best Local Similarly 97.8%; Score 88; DB 4; Length 18;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db

1 KNIRRIIRKIHIKKYG 18

1 KNIRRIIRKIHIKKYG 18

RESULT 2

US-09-840-009-9

Sequence 9, Application US/09840009

Patent No. 6492328

GENERAL INFORMATION:

APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.

APPLICANT: Tack, Brian F.

TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES

FILE REFERENCE: 06510-195WO

CURRENT APPLICATION NUMBER: US/09/840,009

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:52:41 ; Search time 101 Seconds
(without alignments)
68.928 Million cell updates/sec

Title: US-09-642-744D-7

Sequence: 1 KNIRRIKRIHIKKYG 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneeqp19806:*
2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20038:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	AAB70654
2	90	100.0	18	5	ABP53278
3	90	100.0	18	5	ABP53277
4	90	100.0	20	4	AAB70653
5	88	97.8	18	4	AAB70655
6	88	97.8	18	4	AAB70648
7	88	97.8	18	5	AAB70682
8	88	97.8	18	5	AAB70685
9	88	97.8	18	5	AAB70684
10	88	97.8	18	5	AAB70681
11	88	97.8	18	5	AAB70686
12	88	97.8	18	5	ABP53276
13	88	97.8	18	5	ABP53279
14	88	97.8	29	4	AAB70675
15	88	97.8	29	5	ABP53275
16	83	92.2	18	5	AAB70670
17	83	92.2	18	5	AAB70680
18	83	92.2	18	5	AAB70681
19	83	92.2	18	5	AAB70687
20	83	92.2	18	5	AAB70683
21	83	92.2	18	5	AAB70684
22	83	92.2	18	5	AAB70685
23	83	92.2	18	5	AAB70687
24	83	92.2	18	5	ABP53292
25	82	91.1	18	5	AAB70684

26	82	91.1	18	5	AAB70687	AAB70687
27	82	91.1	18	5	AAB70687	AAB70687
28	82	91.1	18	5	AAB70687	AAB70687
29	81	90.0	18	5	AAB70687	AAB70687
30	81	90.0	18	5	AAB70687	AAB70687
31	81	90.0	18	5	AAB70687	AAB70687
32	81	90.0	18	5	AAB70687	AAB70687
33	81	90.0	18	5	AAB70687	AAB70687
34	81	90.0	18	5	AAB70687	AAB70687
35	81	90.0	18	5	AAB70687	AAB70687
36	81	90.0	18	5	AAB70687	AAB70687
37	80	88.9	18	5	AAB70687	AAB70687
38	80	88.9	18	5	AAB70687	AAB70687
39	80	88.9	18	5	AAB70687	AAB70687
40	80	88.9	18	5	AAB70687	AAB70687
41	80	88.9	18	5	AAB70687	AAB70687
42	80	88.9	18	5	AAB70687	AAB70687
43	80	88.9	18	5	AAB70687	AAB70687
44	80	88.9	18	5	AAB70687	AAB70687
45	80	88.9	36	8	ADQ15575	ADQ15575

ALIGNMENTS

RESULT 1

ID AAB70654 standard; peptide; 18 AA.

XX AAB70654;

DT 15-MAY-2001 (first entry)

XX Ovine SMAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:7.

XX Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;

XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;

XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

XX Burkholderia cepacia; Alcaligenes; Xanthomonas.

XX Ovis aries.

XX WO200112668-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022781.

XX 18-AUG-1999; 99US-0149886P.

XX (IOWA) UNIV IOWA RES FOUND.

XX (REGC) UNIV CALIFORNIA.

XX Tack BE, McCreary P, Welsh M, Travis SM, Lehrer R;

XX MPI; 2001-234911/24.

XX New antimicrobial peptides useful as antibiotics for inhibiting growth

XX and proliferation of microbes, and for treating microbial infections.

Claim 1, Page 103; 137pp; English.

AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
antimicrobial and antiviral activities, and can be used as microbial
growth and proliferation inhibitors and in gene therapy. (I) are useful
for inhibiting microbial growth in an environment capable of sustaining
such growth, for inhibiting microbial growth or strain in a host, and
inhibiting the growth of drug-resistant microbial strains such as
Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51; Search time 93.3333 Seconds
(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744D-6
Perfect score: 90
Sequence: 1 KNIRRIIRKIRIKYK 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	61.1	160	1	SCS1_SHEEP
2	55	61.1	160	1	P49928 ovis aries
3	52	57.8	146	2	SCS2_SHEEP
4	49	54.4	2017	2	O9A1H3
5	48.5	53.9	314	2	O675T1
6	48.5	53.9	324	2	O651T6
7	48	53.3	235	2	O62X75
8	48	53.3	235	2	O9LJW2
9	47	52.2	500	1	TF3B_SCHPO
10	47	52.2	232	2	O7MT01
11	47	52.2	581	2	O6EBB6
12	47	52.2	3267	2	O81B20
13	46	51.1	93	2	O64D16
14	46	51.1	113	2	O703Z0
15	46	51.1	250	2	O6L7F9
16	46	51.1	282	2	O8DYR3
17	46	51.1	282	2	O8E4C0
18	46	51.1	319	2	O05804
19	46	51.1	343	2	O76CZ2
20	46	51.1	807	1	HISB_PHOUL
21	46	51.1	1774	2	O754J8
22	45.5	50.6	2084	2	O81LJ6
23	45.5	50.6	208	1	TRPF_NEIMA
24	45.5	50.0	192	2	O896E1
25	45	50.0	192	2	O896E1
26	45	50.0	308	2	O896E1
27	45	50.0	420	1	PRIL_HUMAN
28	45	50.0	609	2	O72WZ1
29	45	50.0	609	2	O8E908
30	45	50.0	647	2	O62647
31	45	50.0	834	2	O7RRI0

ALIGNMENTS

32	45	50.0	1160	2	O81M12
33	45	50.0	1634	2	DBOL_METUA
34	44	48.9	78	2	O82YK7
35	44	48.9	93	1	V435_METUA
36	44	48.9	124	2	O649W3
37	44	48.9	125	2	O64EA5
38	44	48.9	165	2	O81B86
39	44	48.9	231	2	O8R4G4
40	44	48.9	233	2	O8L7X2
41	44	48.9	291	2	O738Z6
42	44	48.9	301	2	O6H2B4
43	44	48.9	301	2	O63BX5
44	44	48.9	301	2	O81E24
45	44	48.9	301	2	O81E24

RESULT 1
SCS1_SHEEP
ID -SCS1_SHEEP STANDARD; PRT; 160 AA.

AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29)
DE 29) (Myeloid antibacterial peptide SWAP-29).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_Taxid:9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RA Mahoney M.M., Lee A.Y., Brezinski-Caligiuri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel
antimicrobial peptide.";
RL PNAS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Huttner K.M., Mahoney M.M.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RT -1- FUNCTION: Thermolabile, broad spectrum, bactericidal agent.
RT -1- SUBCELLULAR LOCATION: Secreted.
RT -1- SIMILARITY: Belongs to the cathelicidin family.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X29757; CAA63412.1; -
CC EMBL: U60600; AAB49715.1; -
CC PDB: 1FRV; NMR: A=132-160.
CC InterPro: IPR001894; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC PROSITE: PS00946; CATHELICIDINS_1; 1.
CC PROSITE: PS00947; CATHELICIDINS_2; 1.
CC 3D-structure: Antibiotic; Pyrolytic; Pyrolytic carboxylic acid; Signal.
CC SIGNAL
CC PROPEP
CC PEPTIDE 30 131
CC MOD_RES 132 160
CC MOD_RES 30 30
CC
CC DISULFID 86 97
CC
CC By similarity.
CC Cathelin-related peptide SCS.
CC Pyrolytic carboxylic acid (By
CC similarity).
CC By similarity.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:01:37 ; Search time 19 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-642-744D-6
Perfect score: 90
Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	61.1	152	2	S68411 cathelin-related p
2	55	61.1	160	2	S68412 cathelin-related p
3	55	61.1	160	2	S68428 myeloid antimicrob
4	46	51.1	319	1	S19248 RNA-directed DNA p
5	45.5	50.6	208	2	G81169 N-(5'-phosphoribos
6	45.5	50.6	208	2	E81935 probable phosphori
7	45	50.0	234	2	D97106 DNA-dependent RNA
8	45	50.0	234	2	I40822 sigk protein - Cio
9	45	50.0	420	2	E45630 DNA primase chain
10	45	50.0	1634	2	E64410 DNA-directed DNA p
11	44	48.9	96	2	C64354 hypothetical prote
12	44	48.9	483	2	S75369 hypothetical prote
13	44	48.9	540	2	T33982 hypothetical prote
14	44	48.9	1670	2	T06754 DNA-directed RNA p
15	43.5	48.3	381	1	C64416 conserved hypotet
16	43	47.8	210	2	AC1577 precortin isomeras
17	43	47.8	417	2	A33269 DNA primase (EC 2.
18	43	47.8	867	2	G69485 DNA-directed RNA p
19	43	47.8	1524	2	G84721 hypothetical prote
20	42	46.7	125	2	A89114 hypothetical prote
21	42	46.7	146	2	D90581 conserved hypotet
22	42	46.7	168	2	T08831 conserved hypotet
23	42	46.7	186	2	B90116 hypothetical prote
24	42	46.7	406	2	A71965 hypothetical prote
25	42	46.7	537	2	C90389 conserved hypotet
26	42	46.7	698	2	D64084 helicas (EC 3.6.1
27	42	46.7	849	2	A96592 hypothetical prote
28	41.5	46.1	483	2	B82160 hypothetical prote
29	41	45.6	108	2	C64490 hypothetical prote

30	41	45.6	117	2	T12722 hypothetical prote
31	41	45.6	152	2	A7285 arginine repressor
32	41	45.6	162	1	A53484 interleukin-15 pre
33	41	45.6	190	2	UC4514 TADA-binding prote
34	41	45.6	190	2	A85360 hypothetical prote
35	41	45.6	256	2	A35340 H+-transporting tw
36	41	45.6	277	2	A70158 ABC transporter, A
37	41	45.6	297	2	H70446 UTP-glucose-1-phos
38	41	45.6	337	2	S46010 hypothetical prote
39	41	45.6	358	2	B64309 hypothetical prote
40	41	45.6	507	2	T10753 intestinal DNA rep
41	41	45.6	613	2	F64056 probable ATP-depen
42	41	45.6	686	1	S28050 transforming prote
43	41	45.6	700	1	S01991 transforming prote
44	41	45.6	704	1	S33704 transforming prote
45	41	45.6	821	2	B71229 pyruvate, water di

ALIGNMENTS

RESULT 1

S68411

cathelin-related protein 2 precursor - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.

FEBS Lett. 377, 519-522, 1995

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial f

A/Reference number: S68411, MUID:96140581, PMID:8549789

A/Accession: S68411

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-152 <MAN>

A/Cross-references: EMBL:X92757

C/Genetics:

A:Gene: SC5-2

C/Superfamily: cathelin; cystatin homology

F/1-21/Domain: signal sequence #status predicted <SIG>

F/124-123/Domain: cystatin homology <CVS>

F/21-123/Domain: propeptide #status predicted <PRO>

F/124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match

Best Local Similarity 61.1%; Score 55; DB 2; Length 152;

Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 124 RGLRRLGKRIAHGVKKYG 141

RESULT 2

S68412

cathelin-related protein 1 precursor - sheep

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.

FEBS Lett. 377, 519-522, 1995

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial f

A/Reference number: S68411, MUID:96140581, PMID:8549789

A/Accession: S68412

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <MAN>

A/Cross-references: EMBL:X92758

C/Genetics:

A:Gene: SC5-1

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/22-130/Domain: cystatin homology <CVS>

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 ; Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744d-6

Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppa/US10E_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppa/US10F_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	90	100.0	18	14	US-10-060-102-10
2	90	100.0	18	14	US-10-060-102-11
3	90	100.0	18	15	US-10-721-839-10
4	90	100.0	18	15	US-10-721-839-11
5	88	97.8	18	9	US-09-840-009-2
6	88	97.8	18	9	US-09-840-009-9
7	88	97.8	18	9	US-09-840-009-16
8	88	97.8	18	9	US-09-840-009-23
9	88	97.8	18	9	US-09-840-009-30
10	88	97.8	18	14	US-10-060-102-9
11	88	97.8	18	14	US-10-060-102-12
12	88	97.8	18	15	US-10-721-839-9
13	88	97.8	18	15	US-10-721-839-12

14	88	97.8	29	14	US-10-060-102-8	Sequence 8, Appl1
15	88	97.8	29	15	US-10-721-839-8	Sequence 8, Appl1
16	83	92.2	18	9	US-09-840-009-4	Sequence 4, Appl1
17	83	92.2	18	9	US-09-840-009-8	Sequence 8, Appl1
18	83	92.2	18	9	US-09-840-009-11	Sequence 11, Appl1
19	83	92.2	18	9	US-09-840-009-15	Sequence 15, Appl1
20	83	92.2	18	9	US-09-840-009-18	Sequence 18, Appl1
21	83	92.2	18	9	US-09-840-009-22	Sequence 22, Appl1
22	83	92.2	18	9	US-09-840-009-25	Sequence 25, Appl1
23	83	92.2	18	9	US-09-840-009-29	Sequence 29, Appl1
24	83	92.2	18	14	US-10-060-102-25	Sequence 25, Appl1
25	83	92.2	18	15	US-10-721-839-25	Sequence 25, Appl1
26	82	91.1	18	9	US-09-840-009-5	Sequence 5, Appl1
27	82	91.1	18	9	US-09-840-009-12	Sequence 12, Appl1
28	82	91.1	18	9	US-09-840-009-19	Sequence 19, Appl1
29	82	91.1	18	9	US-09-840-009-26	Sequence 26, Appl1
30	81	90.0	18	9	US-09-840-009-6	Sequence 6, Appl1
31	81	90.0	18	9	US-09-840-009-7	Sequence 7, Appl1
32	81	90.0	18	9	US-09-840-009-13	Sequence 13, Appl1
33	81	90.0	18	9	US-09-840-009-14	Sequence 14, Appl1
34	81	90.0	18	9	US-09-840-009-21	Sequence 21, Appl1
35	81	90.0	18	9	US-09-840-009-20	Sequence 20, Appl1
36	81	90.0	18	9	US-09-840-009-27	Sequence 27, Appl1
37	81	90.0	18	9	US-09-840-009-28	Sequence 28, Appl1
38	80	88.9	18	9	US-09-840-009-3	Sequence 3, Appl1
39	80	88.9	18	9	US-09-840-009-10	Sequence 10, Appl1
40	80	88.9	18	9	US-09-840-009-17	Sequence 17, Appl1
41	80	88.9	18	9	US-09-840-009-24	Sequence 24, Appl1
42	80	88.9	18	9	US-09-840-009-31	Sequence 31, Appl1
43	80	88.9	18	14	US-10-060-102-26	Sequence 26, Appl1
44	80	88.9	18	14	US-10-077-624-17	Sequence 17, Appl1
45	80	88.9	18	15	US-10-721-839-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
US-10-060-102-10
Sequence 10, Application US/10060102
Publication No. US2003022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL.
FILE REFERENCE: IOWA-035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-060-102-10

Query Match 100.0%; Score 90; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KNIRRIIRKIHIIKKYG 18

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32 ; Search time 25.6667 Seconds
(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-6

Sequence: 1 KNIRRIIRKIHIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/PTTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	88	97.8	18 4 US-09-840-009-2	Sequence 2, Appli
2	88	97.8	18 4 US-09-840-009-9	Sequence 9, Appli
3	88	97.8	18 4 US-09-840-009-16	Sequence 16, Appli
4	88	97.8	18 4 US-09-840-009-23	Sequence 23, Appli
5	88	97.8	18 4 US-09-840-009-30	Sequence 30, Appli
6	83	92.2	18 4 US-09-840-009-4	Sequence 4, Appli
7	83	92.2	18 4 US-09-840-009-8	Sequence 8, Appli
8	83	92.2	18 4 US-09-840-009-11	Sequence 11, Appli
9	83	92.2	18 4 US-09-840-009-15	Sequence 15, Appli
10	83	92.2	18 4 US-09-840-009-18	Sequence 18, Appli
11	83	92.2	18 4 US-09-840-009-22	Sequence 22, Appli
12	83	92.2	18 4 US-09-840-009-25	Sequence 25, Appli
13	83	92.2	18 4 US-09-840-009-29	Sequence 29, Appli
14	82	91.1	18 4 US-09-840-009-3	Sequence 3, Appli
15	82	91.1	18 4 US-09-840-009-5	Sequence 5, Appli
16	82	91.1	18 4 US-09-840-009-12	Sequence 12, Appli
17	82	91.1	18 4 US-09-840-009-19	Sequence 19, Appli
18	81	90.0	18 4 US-09-840-009-26	Sequence 26, Appli
19	81	90.0	18 4 US-09-840-009-6	Sequence 6, Appli
20	81	90.0	18 4 US-09-840-009-7	Sequence 7, Appli
21	81	90.0	18 4 US-09-840-009-13	Sequence 13, Appli
22	81	90.0	18 4 US-09-840-009-20	Sequence 20, Appli
23	81	90.0	18 4 US-09-840-009-21	Sequence 21, Appli
24	81	90.0	18 4 US-09-840-009-27	Sequence 27, Appli
25	81	90.0	18 4 US-09-840-009-28	Sequence 28, Appli
26	80	88.9	18 4 US-09-840-009-3	Sequence 3, Appli
27	80	88.9	18 4 US-09-840-009-10	Sequence 10, Appli

28	80	88.9	18 4 US-09-840-009-17	Sequence 17, Appli
29	80	88.9	18 4 US-09-840-009-24	Sequence 24, Appli
30	80	88.9	18 4 US-09-840-009-31	Sequence 31, Appli
31	74	82.2	18 4 US-09-840-009-34	Sequence 34, Appli
32	74	82.2	18 4 US-09-840-009-35	Sequence 35, Appli
33	72	80.0	18 4 US-09-840-009-32	Sequence 32, Appli
34	72	80.0	18 4 US-09-840-009-33	Sequence 33, Appli
35	68	75.6	18 4 US-09-840-009-1	Sequence 1, Appli
36	63	70.0	18 4 US-09-840-009-36	Sequence 36, Appli
37	63	70.0	18 4 US-09-840-009-37	Sequence 37, Appli
38	55	61.1	160 4 US-09-917-340-36	Sequence 36, Appli
39	52	57.8	169 4 US-09-270-767-35466	Sequence 35466, A
40	52	57.8	169 4 US-09-270-767-50623	Sequence 50623, A
41	48	53.3	205 3 US-09-134-001C-4766	Sequence 4766, Ap
42	44	48.9	24 4 US-09-785-059B-5	Sequence 5, Appli
43	44	48.9	36 4 US-09-785-059B-6	Sequence 6, Appli
44	44	48.9	42 4 US-09-785-059B-7	Sequence 7, Appli
45	44	48.9	48 4 US-09-785-059B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match 97.8%; Score 88; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. NO. 3.9e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNIRRIIRKIHIKKYG 18
Db 1 KNIRRIIRKIHIKKYG 18

RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:52:41 ; Search time 101 Seconds

(without alignments)
68.928 Million cell updates/sec

Title: US-09-642-744D-6

Sequence: 1 KNIRRIIRKIIHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Genesegp16dec04:*
2: genesegp19908:*
3: genesegp20008:*
4: genesegp20018:*
5: genesegp20028:*
6: genesegp20038:*
7: genesegp20038:*
8: genesegp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	AAB70654
2	90	100.0	18	5	ABP53278
3	90	100.0	18	5	ABP53278
4	90	100.0	20	4	AAB70653
5	88	97.8	18	4	AAB70655
6	88	97.8	18	4	AAB70648
7	88	97.8	18	5	AAB20882
8	88	97.8	18	5	AAB20875
9	88	97.8	18	5	AAB20854
10	88	97.8	18	5	AAB20861
11	88	97.8	18	5	AAB20868
12	88	97.8	18	5	ABP53276
13	88	97.8	18	5	ABP53279
14	88	97.8	29	4	AAB70675
15	88	97.8	29	4	ABP53275
16	83	92.2	18	5	AAB20870
17	83	92.2	18	5	AAB20860
18	83	92.2	18	5	AAB20881
19	83	92.2	18	5	AAB20867
20	83	92.2	18	5	AAB20874
21	83	92.2	18	5	AAB20877
22	83	92.2	18	5	AAB20856
23	83	92.2	18	5	ABP53292
24	83	92.2	18	5	ABP53292
25	82	91.1	18	5	AAB20864

26	82	91.1	18	5	AAB20871	AAB20871
27	82	91.1	18	5	AAB20878	AAB20878
28	82	91.1	18	5	AAB20857	AAB20857
29	81	90.0	18	5	AAB20872	AAB20872
30	81	90.0	18	5	AAB20873	AAB20873
31	81	90.0	18	5	AAB20858	AAB20858
32	81	90.0	18	5	AAB20866	AAB20866
33	81	90.0	18	5	AAB20879	AAB20879
34	81	90.0	18	5	AAB20865	AAB20865
35	81	90.0	18	5	AAB20880	AAB20880
36	81	90.0	18	5	AAB20859	AAB20859
37	80	88.9	18	5	AAB20862	AAB20862
38	80	88.9	18	5	AAB20876	AAB20876
39	80	88.9	18	5	AAB20883	AAB20883
40	80	88.9	18	5	AAB20869	AAB20869
41	80	88.9	18	5	AAB20855	AAB20855
42	80	88.9	18	5	ABP53293	ABP53293
43	80	88.9	18	6	ABP72293	ABP72293
44	80	88.9	18	8	ADQ15520	ADQ15520
45	80	88.9	36	8	ADQ15575	ADQ15575

ALIGNMENTS

RESULT 1
AAB70654 standard; peptide, 18 AA.
ID AAB70654
XX
AC AAB70654;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO.7.
XX
KW Ovine, SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
FN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149866P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
DR New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PT Claim 1; Page 103; 137pp; English.
XX
PS AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70668 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (I) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51 / Search time 93.333 Seconds

(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744D-1

Sequence: 1 KNLRRIIRKIHKKYK 18

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot_sprot.*
2: uniprot_tramb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	57	63.3	160 1	SCS1_SHEEP
2	57	63.3	160 1	SCS2_SHEEP
3	54	60.0	146 2	O9A1H3
4	50	55.6	255 2	O9LJW2
5	49	54.4	581 2	O6EBB6
6	48	53.3	250 2	O6LFF9
7	48	53.3	500 1	TF3B_SCHPO
8	48	53.3	3267 2	O8IBZ0
9	47	52.2	113 2	O703Z0
10	47	52.2	2017 2	O675F1
11	46.5	51.7	314 2	O62X75
12	46.5	51.7	324 2	O62X75
13	46	51.1	282 2	O8DYR3
14	46	51.1	282 2	O8DYR3
15	46	51.1	319 2	O05804
16	46	51.1	349 2	O736D5
17	46	51.1	349 2	O81P89
18	46	51.1	349 2	O6HMT2
19	46	51.1	684 2	O7QNN1
20	46	51.1	954 2	O9GQI5
21	46	51.1	969 2	O9U022
22	45.5	50.6	381 1	TH11_METUA
23	45	50.0	232 2	O7WMT0
24	45	50.0	308 2	O8R2C7
25	45	50.0	402 2	O8R2C7
26	45	50.0	402 2	O8R2C7
27	45	50.0	402 2	O8R2C7
28	44	48.9	78 2	O82YK7
29	44	48.9	93 2	O64DI6
30	44	48.9	124 2	O649W3
31	44	48.9	125 2	O64EAS

ALIGNMENTS

RESULT 1	ID	SCS1_SHEEP	STANDARD	PRT	160 AA
AC	P49928				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29)				
DE	29) (Myeloid antibacterial peptide SWAP-29)				
OS	Ovis aries (Sheep)				
OC	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	NCBI_TaxID=9940;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;				
RA	Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Hutner K.M.;				
RT	"Molecular analysis of the sheep cathelin family reveals a novel				
RT	antimicrobial peptide."				
RL	FEBS Lett. 377:519-522(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RA	Hutner K.M., Mahoney M.M.;				
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: Thermostable, broad spectrum, bactericidal agent.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: Belongs to the cathelicidin family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL; X52757; CAA63412.1; -				
DR	EMBL; U60600; AAB49715.1; -				
DR	PDB; 1FRY; NMR; A=132-160.				
DR	InterPro; IPR001894; Cathelicidin.				
DR	Pfam; PF00666; Cathelicidin; 1.				
DR	ProDom; PDD01838; Cathelicidin; 1.				
DR	PROSITE; PS00946; CATHELICIDINS 1; 1.				
DR	PROSITE; PS00947; CATHELICIDINS 2; 1.				
KW	3D-structure; Antibiotic; Pyrrolidone carboxylic acid; Signal.				
FT	SIGNAL	1	29		
FT	PROPEP	30	131		
FT	PEPTIDE	132	160		
FT	MOD_RES	30	30		
FT	DISULFID	86	97		

By similarity.
Cathelin-related peptide SCS.
Pyrrolidone carboxylic acid (by similarity).
By similarity.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:01:37 ; Search time 19 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-642-744d-1

Perfect score: 90

Sequence: 1 KNLRRIRKIHIIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	63.3	152	2	S68411
2	57	63.3	160	2	S68412
3	57	63.3	160	2	S68228
4	46	51.1	319	1	S19248
5	45.5	50.6	381	1	C64416
6	45	50.0	1634	2	E64410
7	44	48.9	1670	2	T06754
8	43.5	48.3	208	2	G81169
9	43.5	48.3	208	2	B81935
10	43	47.8	210	2	AC1577
11	43	47.8	234	2	D97108
12	43	47.8	234	2	I40822
13	43	47.8	420	2	S45630
14	43	47.8	537	2	C90389
15	42	46.7	41	2	S77368
16	42	46.7	96	2	C64354
17	42	46.7	125	2	A99114
18	42	46.7	146	2	D90581
19	42	46.7	152	2	A72385
20	42	46.7	168	2	T08831
21	42	46.7	186	2	B90116
22	42	46.7	187	2	H71819
23	42	46.7	359	2	S77322
24	42	46.7	429	2	D90428
25	42	46.7	483	2	S75369
26	42	46.7	507	2	T10753
27	42	46.7	540	2	T33982
28	42	46.7	594	2	D70127
29	42	46.7	698	2	D64084

30	42	46.7	937	2	T37241	olfactory channel
31	42	46.7	957	2	D88651	protein B012.5 (i
32	42	46.7	1741	2	T15978	hypothetical prote
33	41.5	46.1	313	2	A89971	cmp-binding-factor
34	41	45.6	117	2	T12722	hypothetical prote
35	41	45.6	181	2	B90246	TATA box binding p
36	41	45.6	190	2	A85360	hypothetical prote
37	41	45.6	198	2	S55311	hypothetical prote
38	41	45.6	207	2	E70407	TATA-binding prote
39	41	45.6	256	2	A35340	probable CDP-alcoh
40	41	45.6	297	2	H70446	H+-transporting tw
41	41	45.6	337	2	S46010	urp-glucose-1-phos
42	41	45.6	338	2	D90017	hypothetical prote
43	41	45.6	367	2	S19172	hypothetical prote
44	41	45.6	414	2	G64091	cytochrome P450 2B
45	41	45.6	417	2	A33269	cell division prot
						DNA primase (EC 2.

ALIGNMENTS

RESULT 1

S68411

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S68411

R:Mahoney, M.M., Lee, A.Y., Brezinski-Caliguri, D.J., Huttnet, K.M.

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial i

A:Reference number: S68411; MUID:96140581; PMID:8549789

A:Accession: S68411

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-152 <MAH>

A:Cross-references: EMBL:X92757

C:Gene: SCS-2

C:Superfamily: cathelin; cystatin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:14-122/Domain: cystatin homology <CYS>

F:21-123/Domain: propeptide #status predicted <PRO>

F:124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match 63.3%; Score 57; DB 2; Length 152;
Best Local Similarity 61.1%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KNLRRIRKIHIIKKYG 18

DB 124 RGLRLRGKIHAGVKKYG 141

RESULT 2

S68412

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S68412

R:Mahoney, M.M., Lee, A.Y., Brezinski-Caliguri, D.J., Huttnet, K.M.

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial i

A:Reference number: S68411; MUID:96140581; PMID:8549789

A:Accession: S68412

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-160 <MAH>

A:Cross-references: EMBL:X92758

C:Gene: SCS-1

C:Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:122-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 ; Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744D-1

Perfect score: 1 KNLRRIRKIIHIKYG 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	18	9	US-09-840-009-2
2	90	100.0	18	9	US-09-840-009-9
3	90	100.0	18	9	US-09-840-009-16
4	90	100.0	18	9	US-09-840-009-23
5	90	100.0	18	9	US-09-840-009-30
6	90	100.0	18	14	US-10-060-102-9
7	90	100.0	18	14	US-10-060-102-12
8	90	100.0	18	15	US-10-721-839-9
9	90	100.0	18	15	US-10-721-839-12
10	90	100.0	29	14	US-10-060-102-8
11	90	100.0	29	15	US-10-721-839-8
12	88	97.8	18	14	US-10-060-102-10
13	88	97.8	18	14	US-10-060-102-11

14	88	97.8	18	15	US-10-721-839-10	Sequence 10, Appl
15	88	97.8	18	15	US-10-721-839-11	Sequence 11, Appl
16	85	94.4	18	9	US-09-840-009-4	Sequence 4, Appl
17	85	94.4	18	9	US-09-840-009-8	Sequence 8, Appl
18	85	94.4	18	9	US-09-840-009-11	Sequence 11, Appl
19	85	94.4	18	9	US-09-840-009-15	Sequence 15, Appl
20	85	94.4	18	9	US-09-840-009-18	Sequence 18, Appl
21	85	94.4	18	9	US-09-840-009-22	Sequence 22, Appl
22	85	94.4	18	9	US-09-840-009-25	Sequence 25, Appl
23	85	94.4	18	9	US-09-840-009-29	Sequence 29, Appl
24	85	94.4	18	14	US-10-060-102-25	Sequence 25, Appl
25	85	94.4	18	15	US-10-721-839-25	Sequence 25, Appl
26	84	93.3	18	9	US-09-840-009-5	Sequence 5, Appl
27	84	93.3	18	9	US-09-840-009-12	Sequence 12, Appl
28	84	93.3	18	9	US-09-840-009-19	Sequence 19, Appl
29	84	93.3	18	9	US-09-840-009-26	Sequence 26, Appl
30	83	92.2	18	9	US-09-840-009-6	Sequence 6, Appl
31	83	92.2	18	9	US-09-840-009-7	Sequence 7, Appl
32	83	92.2	18	9	US-09-840-009-13	Sequence 13, Appl
33	83	92.2	18	9	US-09-840-009-14	Sequence 14, Appl
34	83	92.2	18	9	US-09-840-009-20	Sequence 20, Appl
35	83	92.2	18	9	US-09-840-009-21	Sequence 21, Appl
36	83	92.2	18	9	US-09-840-009-27	Sequence 27, Appl
37	83	92.2	18	9	US-09-840-009-28	Sequence 28, Appl
38	82	91.1	18	9	US-09-840-009-3	Sequence 3, Appl
39	82	91.1	18	9	US-09-840-009-10	Sequence 10, Appl
40	82	91.1	18	9	US-09-840-009-17	Sequence 17, Appl
41	82	91.1	18	9	US-09-840-009-24	Sequence 24, Appl
42	82	91.1	18	9	US-09-840-009-31	Sequence 31, Appl
43	82	91.1	18	14	US-10-060-102-26	Sequence 26, Appl
44	82	91.1	18	14	US-10-077-624-17	Sequence 17, Appl
45	82	91.1	18	15	US-10-721-839-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. US20020082195A1
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVEL PEPTIDES
FILE REFERENCE: 06510-1950
CURRENT APPLICATION NUMBER: US/09/840, 009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606, 858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match 100.0%; Score 90; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNLRRIRKIIHIKYG 18
DB 1 KNLRRIRKIIHIKYG 18

RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32; Search time 25.6667 Seconds
(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-1

Perfect score: 90

Sequence: 1 KNLRRIIRKIHIKKYG 18

Scoring table:

BLOSUM62

Searched:

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	US-09-840-009-2
2	90	100.0	18	4	US-09-840-009-9
3	90	100.0	18	4	US-09-840-009-15
4	90	100.0	18	4	US-09-840-009-23
5	90	100.0	18	4	US-09-840-009-30
6	85	94.4	18	4	US-09-840-009-4
7	85	94.4	18	4	US-09-840-009-8
8	85	94.4	18	4	US-09-840-009-11
9	85	94.4	18	4	US-09-840-009-15
10	85	94.4	18	4	US-09-840-009-18
11	85	94.4	18	4	US-09-840-009-22
12	85	94.4	18	4	US-09-840-009-25
13	85	94.4	18	4	US-09-840-009-29
14	84	93.3	18	4	US-09-840-009-5
15	84	93.3	18	4	US-09-840-009-12
16	84	93.3	18	4	US-09-840-009-19
17	84	93.3	18	4	US-09-840-009-26
18	83	92.2	18	4	US-09-840-009-6
19	83	92.2	18	4	US-09-840-009-7
20	83	92.2	18	4	US-09-840-009-13
21	83	92.2	18	4	US-09-840-009-14
22	83	92.2	18	4	US-09-840-009-20
23	83	92.2	18	4	US-09-840-009-21
24	83	92.2	18	4	US-09-840-009-27
25	83	92.2	18	4	US-09-840-009-28
26	82	91.1	18	4	US-09-840-009-3
27	82	91.1	18	4	US-09-840-009-10

28	82	91.1	18	4	US-09-840-009-17	Sequence 17, Appl
29	82	91.1	18	4	US-09-840-009-24	Sequence 24, Appl
30	82	91.1	18	4	US-09-840-009-31	Sequence 31, Appl
31	76	84.4	18	4	US-09-840-009-34	Sequence 34, Appl
32	76	84.4	18	4	US-09-840-009-35	Sequence 35, Appl
33	74	82.2	18	4	US-09-840-009-32	Sequence 32, Appl
34	74	82.2	18	4	US-09-840-009-33	Sequence 33, Appl
35	70	77.8	18	4	US-09-840-009-1	Sequence 1, Appl
36	65	72.2	18	4	US-09-840-009-36	Sequence 36, Appl
37	65	72.2	18	4	US-09-840-009-37	Sequence 37, Appl
38	57	63.3	160	4	US-09-917-340-36	Sequence 37, Appl
39	50	55.6	169	4	US-09-270-767-35406	Sequence 36, Appl
40	50	55.6	169	4	US-09-270-767-50623	Sequence 35406, A
41	50	55.6	205	3	US-09-134-001C-4766	Sequence 4766, Ap
42	43.5	48.3	167	4	US-09-710-279-1502	Sequence 1502, Ap
43	43.5	48.3	320	3	US-09-134-001C-3823	Sequence 3823, Ap
44	43	47.8	823	4	US-09-949-016-8339	Sequence 8339, Ap
45	42	46.7	24	4	US-09-785-059B-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Wang, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match      100.0%; Score 90; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 KNLRRIIRKIHIKKYG 18
Db      1 KNLRRIIRKIHIKKYG 18

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Wang, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:52:41 ; Search time 101 Seconds
(without alignments)
68.928 Million cell updates/sec

Title: US-09-642-744d-1

Perfect score: 90

Sequence: 1 KMLRRIRKIHITKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
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2: geneseqp19808:*
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6: geneseqp20038:*
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8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	AAB70655
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5	90	100.0	18	5	AAE20864
6	90	100.0	18	5	AAE20861
7	90	100.0	18	5	AAE20868
8	90	100.0	18	5	ABP53276
9	90	100.0	18	5	ABP53279
10	90	100.0	29	4	AAE20875
11	90	100.0	29	5	ABP53275
12	88	97.8	18	4	AAE20864
13	88	97.8	18	5	ABP53278
14	88	97.8	18	5	ABP53277
15	88	97.8	20	4	AAE20863
16	85	94.4	18	5	AAE20870
17	85	94.4	18	5	AAE20860
18	85	94.4	18	5	AAE20881
19	85	94.4	18	5	AAE20867
20	85	94.4	18	5	AAE20874
21	85	94.4	18	5	AAE20863
22	85	94.4	18	5	AAE20877
23	85	94.4	18	5	AAE20856
24	85	94.4	18	5	ABP53292
25	84	93.3	18	5	AAE20864

26	84	93.3	18	5	AAE20871	AAE20871 S10-novis
27	84	93.3	18	5	AAE20878	AAE20878 S11-novis
28	84	93.3	18	5	AAE20857	AAE20857 S6-novisp
29	83	92.2	18	5	AAE20872	AAE20872 E10-novis
30	83	92.2	18	5	AAE20873	AAE20873 D10-novis
31	83	92.2	18	5	AAE20858	AAE20858 E6-novisp
32	83	92.2	18	5	AAE20866	AAE20866 D7-novisp
33	83	92.2	18	5	AAE20879	AAE20879 E11-novis
34	83	92.2	18	5	AAE20865	AAE20865 D11-novis
35	83	92.2	18	5	AAE20880	AAE20880 D11-novis
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42	82	91.1	18	5	ABP53293	ABP53293 Synthetic
43	82	91.1	18	6	ABP72293	ABP72293 Antimicro
44	82	91.1	18	8	ADQ15520	ADQ15520 Antimicro
45	82	91.1	36	8	ADQ15575	ADQ15575 Novipitri

ALIGNMENTS

RESULT 1
ID AAB70655 standard; peptide; 18 AA.
XX
AC AAB70655;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:8.
XX
KW Ovine: SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-019886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccravy P, Welsh M, Travis SM, Lehrner R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (1), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (1) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas